

FIGURE 1

GGACTAATCTGTGGGAGCAGTTATTCCAGTATCACCCAGGGTGCAGCCACACCAGGACTGT
GTTGAAGGGTGTCCCCCTTAAATGTAATACCTCCTCATCTTTCTTACACAGTG
TCTGAGAACATTACATTATAGATAAGTAGTACATGGTGGATAACTCTACTTTAGGAGGA
CTACTCTTCTGACAGTCCTAGACTGGTCTTACACTAAGACACC**ATGA**AGGAGTATGTG
CTCCTATTATTCTGGCTTGTGCTCGCAAACCCCTTCTTAGCCCTCACACATCGCACT
GAAGAATATGATGCTGAAGGATATGGAAGACACAGATGATGATGATGATGATGATG
ATGATGATGATGAGGACAACTCTTTCCAACAAGAGAGGCCAGAAGCCATTTC
TTTGATCTGTTCCAATGTGCCATTGGATGTCAGTCTATTCAACGAGTTGTACATTGCTC
AGATTTAGGTTGACCTCAGTCCAAACCAACATTCCATTGATACTCGAATGCTTGATCTC
AAAACAATAAAATTAGGAAATCAAAGAAAATGATTTAAAGGACTCACTTCACTTATGGT
CTGATCCTGAACAACAACAAGCTAACGAAGATTCAACCAAAAGCCTTCTAACACAAAGAA
GTTGCGAAGGCTGTATCTGCCCACAATCAACTAAGTGAACATACCACTTAATCTCCAAAT
CATTAGCAGAACTCAGAATTCAATGAAAATAAGTTAAGAAAATACAAAAGGACACATTCAA
GGAATGAATGCTTACACGTTGGAAATGAGTGCAAACCCCTTCTGATAATAATGGATAGA
GCCAGGGCATTGAGGGGTGACGGTGTCCATATCAGAATTGAGCAGAAGCAAAATGACCT
CAGTTCTAAAGGCTTACCAACTTTATTGGAGCTTCACCTAGATTATAATAAAAATTCA
ACAGTGGAACTTGAGGATTAAACGATACAAAGAACTACAAAGGCTGGCCTAGGAAACAA
CAAATCACAGATATCGAAAATGGAGTCTGCTAACATACCACGTGTGAGAGAAATACATT
TGGAAAACAATAAACTAAAAAAATCCCTCAGGATTACCAAGAGTTGAACATCTCCAGATA
ATCTTCCTTCATTCTAATTCAATTGCAAGAGTGGAGTAAATGACTTCTGTCCAACAGTGCC
AAAGATGAAGAAATCTTATACAGTGCAATAAGTTATTCAACAAACCGGTGAAATACTGGG
AAATGCAACCTGCAACATTGTTGTGGAGCAGAATGAGTGTTCAGCTGGAACTTT
GGAATG**TAA**TAATTAGTAATTGTAATGTCCATTAAATATAAGATTCAAAATCCCTACATT
TGGAAACTCTATTAAATAATGGTAGTATTATATACAGCAAAATATCTATTCTCA
AGTGGTAAGTCCACTGACTTATTGACAAGAAATTCAACGGAATTGCAACACTATT
GATACATAAGGGTTGAGAGAAACAGCATCTATTGCAAGTTCTTGTGACAAATGAT
CTTACATAAACTCATGCTTGACCATTCTTCTTCATAACAAAAAGTAAGATATTGCGTA
TTAACACATTGTTATCAAGCACATTAAAAGAACTGTACTGTAATGGAAATGCTTGACT
TAGAAAATTTGCTCTTCATTGCTGTAGAAAACAGAATTAACAAAGACAGTAATGT
GAAGAGTGCATTACACTATTCTTATTGAAACTTGGTAGTACTGTAATATTAAAT
CATCTTAAAGTATGATTGATATAATCTTATTGAAATTACCTTATCATGCTTAGAGCCGT
CTTTATGTTAAAACAATTCTTAAATAAAGCCTCAGTAATGTTCACTTACCAACTTGA
TAAATGCTACTCATAAGAGCTGGTGGGGCTATAGCATATGCTTTTTTTTAATTATT
ACCTGATTAAAATCTCTGTAACAGTGTAGTGTTCATAAAATCTGTAACCTCGCATT
AATGATCCGCTATTATAAGCTTTAATAGCATGAAAATTGTTAGGCTATAAACATTGCCAC
TTCAACTCTAAGGAATATTGAGATATCCCTTGGAAAGACCTGCTTGGAAAGAGCCTGGA
CACTAACAAATTCTACACCAAATTGTCTCTCAAATACGTATGGACTGGATAACTCTGAGAAA
CACATCTAGTATAACTGAATAAGCAGAGCATCAAATTAAACAGACAGAAACGAAAGCTCTA
TATAATGCTCAGAGTTCTTATGTATTGCAACATATGTAACATGAAACAGAAA
ACAGGGAAATTTCATTAAAATATTGGTTGAAAT

FIGURE 2

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA34392
<subunit 1 of 1, 379 aa, 1 stop
<MW: 43302, pI: 7.30, NX(S/T): 1
MKEYVLLLFLALCSAKPFFSPSHIALKNMMLKDMEDDDDDDDDDDDDEDNSLFPTREPR
SHFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGL
TSLYGLILNNNKLTKIHPKAFLTTKLRRLYLSHNQLSEIPLNLPKSLAELRIHENVKKIQ
KDTFKGMNALHVLEMSANPLDNNGIEPGAFEGVTVFHIRIAEAKLTSVPKGLPPTLLELHLD
YNKISTVELEDFKRYKELQRLGLGNNKITDIENGLANIPRVREIHLENNKLKKIPSGLPEL
KYLQIIFLHSNSIARGVNDFCPTVPKMKSLYSAISLFNNPVKYWEMQPATFRCVLSRMSV
QLGNFGM

Signal sequence.

amino acids 1-15

N-glycosylation site.

amino acids 281-285

N-myristoylation sites.

amino acids 129-135, 210-216, 214-220, 237-243, 270-276, 282-288

Leucine zipper pattern.

amino acids 154-176

FIGURE 3

CGGACGCGTGGCGGACCGTGGGCCCGCGCACCGCCCCGGCCCTCCGCCCTCCGACTCGCGCTCC
CTCCCTCCGCCGCTCCCGCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCC
GGCCCCGCCGGCCCCGCTGCTGCTCCTCGGGCTGCTGCTCGGCTCCGGCCGGCCGGCCGGCCGG
GCCCCCCGTGCTGCCCATCCGTTCTGAGAAGGAGCCGCTGCCGTTCGGGGAGCGGCAGGCTGCACCTTCGGCG
GAAGGTCTATGCCCTGGACGAGACGTGGCACCCGGACCTAGGGCAGCCATTGGGGTATGCGCTGCGTGTG
CGCCTGCGAGGCGCCTCAGTGGGTGCGCGTACAGGGCCCTGGCAGGGTCAGCTGCAAGAACATCAA
GTGCCCCAACCCCGGCTGTGGGAGCCGAGCCGGCAGCTGCCGGACACTGCTGCAGACCTGCC
CAGTTCGGAGCGGAGCCGAGCGGGCTGCTCGAGTATCCGGGACCCGGAGCATTGCAAGTTAGCGACCC
CGGGGAGCCAGGGCGTGAAGGAGCGGGCCGTGGTGACGCCACAGGACTTCGCTGGCCTGCTGACAGGGCGAG
GTCGCAAGGGGGCTGGCACGAGCCGAGTCTGCTGCTGCGCTCTAGGCTCCGCTCTATCTCCTACAGGGCGCT
GGACCGCCCTACCAGGATCCGCTTCTCAGACTCCAATGGCAGTGTCTGTTGAGCACCTGCAGCCCCACCA
AGATGGCCTGGTCTGTGGGTGTGGCGGGAGTGCCTCGGTTGCTCTGCGGCTCCTAGGGCAGAACAGCTGCA
TGTGGCACTTGTGACACTCACTCACCCCTCAGGGGAGGTCTGGGGCCTCTCATCCGGCACCGGGCCTGGCTGC
AGAGACCTCAGTGCATCCTGACTCTAGAAGGCCCCCACAGCAGGGCGTAGGGGCATCACCTGCTCACTCT
CAGTGACACAGAGGACTCCTGCTTTTGCTGCTCTCCGAGGGCTGCTGGAACCCAGGAGTGGGGACTAAC
CCAGGTTCCCTTGAGGCTCCAGATTCTACACCAGGGCAGCTACTGCGAGAACCTCAGGCCATGCTCAGCCA
GGAACCAGGCTTGTGAGGTGCTGCCAACCTGACAGTCCAGGAGATGGACTGGCTGGTGCTGGGGAGCTGCA
GATGGCCCTGGAGTGGCAGGCCAGGGCTGCGCATCAGTGGACACATTGCTGCCAGGAAGAGCTGCGACGT
CCTGCAAAGTGTCTTGTGGGCTGATGCCCTGATCCAGTCCAGGGTGCTGCCGCTCAGCAGCCTCAC
GCTGCTAGGAAATGGCTCCCTGATCTATCAGGTGCAAGTGGTAGGGACAAGCAGTGAGGTGGTGCCATGACACT
GGAGACCAAGGCTCAGCGGAGGGATCAGCGACTGCTCTGCCCCATGGCTGGACTCCAGCCAGGAGGACAC
GGCCGTGGTATCTGCCCTGGCTGGCGCCAGGGCTCATATGCTGCTGAGAATGAGCTTCTGAAACGT
GGGCACCAAGGACTTCCAGCGGAGAGCTTCGGGGCACGTGGCTGCCCTGCCCTACTGTGGCATAGGCCCG
CCATGACACGCTGCCGTGCCCTAGCAGGCCCTGGTGAAGAGCCAAGCAGCAGGGCACCG
CTGGCTTCTTGTGATAACCACTGTCACCTGCACTATGAAGTGCTGCTGGCTGGCTGGCTGAGAACAGG
CACTGTCACTGCCACCTCCTGGCCTCCTGGAAACGCCAGGGCTCGGCGGTGCTGAAGGATTCTATGGCTC
AGAGGCCAGGGTGTGGTGAAGGACCTGGAGGCCAGCTGCTGCCACCTGGCAAAAGGCATGGCTCCCTGAT
GATCACCACCAAGGGTAGCCCCAGAGGGAGCTCCGAGGGCAGGTGCAATAGCCAACCAATGTGAGGTGGCGG
ACTGCGCTGGAGGCCGGGGCGAGGGGGTGCAGGGCTGGCTGGCTCCGGATACAGCCTCTGCTGCGCCGCC
TGTGGTGCCTGGCTCCGGCCCTAGGCCCGCAAACCTGGTGGCTGGGGGGGGAGAACCCAAACACATG
CTTCTTGAGGGCAGCGAGGCCAACGGGCTCGTGGCGCCAACACTAGACCCGCTCTGCTCACTCTGCA
CTGCCAGAGACGAACGGTGTGATCTGTCACCGGGTGGTGTGCCACGGCCAGCTGCCACACCGGTGCAGGCTCC
CGACCAAGTGTGCCCTGTTGCCCTGAGAAACAAGATGTCAGAGACTTGCCAGGGCTGCAAGGAGCCGGGACCC
AGGAGAGGGCTGCTATTGATGGTACCGGAGCTGGGGCAGGGGTACGGTGGCACCCGGTGTGCCCC
CTTGGCTTAATTAAGTGTGCTGTCACCTGCAAGGGGGCACTGGAGAGGTGACTGTGAGAAGGTGCAAGT
TCCCCGGCTGGCTGTGCCACGCCCTGAGCTGCTGTCACCCACTGCTGCAAAACAGTGTCCAGTGGGTGCGG
GCCCAACCCAGCTGGGGACCCATGCAGGCTGATGGGCCCGGGCTGCCGTTTGTGGCTGGGAGTGGTCCC
AGAGAGTCAGAGCTGGCACCCCTCAGTGCCCTTTGGAGAGATGAGCTGTATCACCTGCAAGATGTGGGGAGG
GGTGCCTCACTGTGAGCGGGATGACTGTTCACTGCCACTGCTCTGCTGGCTGGGAAGGGAGAGTCGATGCTGTT
CCGCTGCACGGCCACCCGGCCGGCCCCAGAGACCAGAACCTGATCCAGAGCTGGAGAAAGAACCGGAAGGCTCTA
GGGAGCAGCCAGAGGGCAAGTGCACCAAGAGGATGGGCCGAGCTGGGGAGGGGTGGCATCGAGAACCTTCT
GCATTCTCCTGTGGGAAGGCCAGTGCCTTGTCTGCTCTGCTGCTACTCCACCCCAACTACCTCTGGGAA
CCACAGCTCCACAAGGGGGAGAGGCCAGCTGGGCCAGACCGAGGTACAGCCACTCCAAGTCCCTGCCCTGCC
TCGGCCTCTGCTCTGGAAAGCCCCACCCCTTCTCTGTACATAATGTCACTGGCTGTGGGATTAAATT
TCTTCACTCAGCACCAAGGGCCCCGACACTCCACTCTGCTGCCCTGAGCTGAGCAGAGTCATTATTGGAGAG
TTTGTATTATTAAACATTCTTTCACTCAAAAAAAAAAAAAAA

FIGURE 4

><subunit 1 of 1, 954 aa, 1 stop

><MW: 101960, pI: 8.21, NX(S/T): 5

MPSLPPAPPLLLGLLLLGSRPARGAGPEPPVLPIRSEKEPLPVRAAGCTFGGKVYALDE
TWHPDLGQPGVMRCVLCACEAPQWGRRTGPGRVSKNIKPECPPTACGQPRQLPGHCCQT
CPQERSSSERQPSGLSFEYPRDPEHRSYSDRGEPEGAERARGDHTDFVALLTGP
RSQAVARARVSLLRSSLRFSISYRRLDRPTRIRFSDSNGSVLFEH
PAAPTQDGLVCGVWR
AVPRLSRL
LRAEQLHVALVTLTHPSGEVWGPLIRH
RALAAETFSAILTLEGPPQQGVGGITLLTLS
TEDSLHFLLLFRGLLEPRSGGLTQVPLRLQI
LHQGQLLRELQANVSAQEPEGFAEVLPNLT
VQEMDWLVLGELOQMALEWAGRPG
LRI
SGHIAARKSCDVLQS
VLCGADALIPV
QTGAAGSASL
TLLGN
GSLIYQVQVVG
TSSEVVAMT
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Signal sequence.

amino acids 1-23

N-glycosylation sites.

amino acids 217-221, 351-355, 365-369, 434-438

Tyrosine kinase phosphorylation sites.

amino acids 145-153, 778-786

N-myristoylation sites.

amino acids 20-26, 47-53, 50-56, 69-75, 73-79, 232-238, 236-242, 390-396, 422-428, 473-479, 477-483, 483-489, 489-495, 573-579, 576-582, 580-586, 635-641, 670-676, 773-779, 807-813, 871-877, 905-911

Amidation site.

amino acids 87-91

Cell attachment sequence.

amino acids 165-168

Leucine zipper pattern

amino acids 315-337

FIGURE 5

GGCGGAGCAGCCCTAGCCGCCACCGTCGCTCTCGCAGCTCTCGGCCACTGCCACCGCCGCCGCGTCAGCTGC
TCCTGGCTCCGGCTCCCGCCCTCCGGCCATGCCAGCCCCGCCGCCAGCGCCGGTGCAGCTGC
TGCCCGCGCTGGCCCTGCTGCTGCTGCTGGAGCGGGGCCCGAGGCAGCTCCCTGGCCAACCGGTGCCCG
CCGGCCCTTGTGCGCCCCGGCGTGCAGCCCTGGCAAGGGAAATGGGGGTGTCAGCTGCCACCTCGGCCCTG
AGCCGGACCCGAGCACCCGGCCCCGCCGGCTGGCTACAGCTGCACCTGCCCGGGATCTCCGGCG
CCAAGTGCAGCTTGTGAGATCCTTGCCAGCAACCCCTTGTCAACATGGCAACTGCAGCAGCAGCAGCA
GCAGCAGCAGTGGCTACCTCTGCAATTGCAATGAAGGCTATGAAGGTCCAACGTGAACAGGACTTCCAGTC
TCCCAGCCACTGGCTGGACCGAATCCATGGCACCCGACAGCTTCAGCTGTTCTGCTACTCAGGAGCTGACA
AAATCCTGCCTCGCTCTCAGGCAACGGTGAACACTGCCTACCTGGCAGCCAAAACAGGGCAGAAAGTTGAGAAA
TGAAATGGATCAAGTGGAGGTGATCCCAGATATTGCGCTGGGAATGCCAGTTCTAACAGCTCTGGGGTGGCC
GCCTGGTATCCTTGAAGTGCCACAGAACACCTCAGTCAAGATTGCCACTGCCTCACTGATTG
TCTGGAAGGTACGGCCACAGGATTCCAACAGTGCCTCCCTCATAGATGGACGAAGTGTGACCCCCCTTCAGGCTT
CAGGGGACTGGCTCCTGGAGGAGATGCTGCCCTGGGAATAATCATTATTGGTTTGTGAATGATTCTG
TGACTAAGTCTATTGCGCTTAACCTGGTGGTGAAGGTCAACCTGTCAGCAGTGCCTGGGGAGAGTCACG
CAAATGACTTGGAGTGTTCAGGAAAAGGAAATGCAACCGAAGCCGTCAAGAGGCAACTTTTCTGTAACCTG
AGGAGCAGTACGTGGGTAATTCTGTGAAGAATACGATGCTTGCAGAGGAAACCTGCCAAAACAACGCCAGCT
GTATTGATGCAAATGAAAAGCAAGATGGAGCAATTTCACCTGTTGCTTGCCTTCTGGTTAACTGGAGAGCTTT
GCCAGTCCAAGATTGATTACTGCATCCTAGACCCATGCAGAAATGGAGCAACATGCATTCCAGTCTCAGTGGAT
TCACCTGCCAGTGTCCAGAAGGATACTTCGGATCTGCTTGTGAAGAAAAGGTGGACCCCTGCCCTCGTCTCCGT
GCCAGAACACGGCACCTGCTATGTGGACGGGTACACTTACCTGCAACTGCAGCCGGCTCACAGGGCCGA
CCTGTGCCAGCTTATTGACTTCTGTGCCCTCAGCCCTGTGCTCATGGCACGTGCCAGCGTGGGACACAGCT
ACAAATGCCCTGTGATCCAGGTACCATGGCTCTACTGTGAGGAGGAATATAATGAGTGCCTCTCGCTCCAT
GCCGAATGCAGCCACCTGCAGGGACCTCGTTAATGGCTATGAGTGTGTCCTGGCAGAATACAAAGGAACAC
ACTGTGAATTGTACAAGGATCCCTGCGTAACGTCAGCTGTAACGGAGCCACCTGTGACAGCGACGGCTGA
ATGGCACGTGCATCTGTGCACTGGGTTACAGGTGAAGAGTGCACATTGACATAATGAATGTGACAGTAACC
CCTGCCACCATGGGGAGCTGCCCTGGACCAAGCCAAATGGTTATAACTGCCACTGCCGATGTTGGGGAG
CAAACGTGAGATCCACCTCCAATGGAAGTCCGGGACATGCCGAGAGCCTACCAACATGCCACGGCCTCC
TCTACATCATCATTGGAGCCCTCTGCTGGCTTACCTTATGCTGATCATCTGATCGTGGGATTGCCGCA
TCAGCCGATTGAATACCAGGGTCTCCAGGCCAGCCTATGAGGAGTCTACAACGCCAGCATCGACAGCG
AGTTCAGCAATGCATTGCATCCATCCGGCATGCCAGGTTGGAAAGAAATCCGGCTGCAATGTATGATGTGA
GCCCATGCCCTATGAAGATTACAGTCTGATGACAACCCCTGGTCACACTGATTAAACTAAAGATTGTAAT
CTTTTTGGATTATTTCAAAAAGATGAGACTACACTCATTTAAATTTTAAGAAAATAAAAGCTAA
GAAATTAAAATGCTAGCTGCTCAAGAGTTTCACTGAGAATATTAAAGAAACTAATTCTGCACTTGTG
GAAAAAATATTAAAACAAAATTGTGAAACCTATAGACCGATGTTTAATGTAACCTCAGCTCTAAACTGT
GTGCTTCACTAGTGTGCTTTCACTGTAGACACTATCACGAGACCCAGATTAATTCTGTTGTTACA
GAATAAGTCTAACGAGAGAAGTCTGTTGACGTTGAGTGCCTTCTGAGTAGAGTTAGAAAACCAC
GTAACGTAGCATATGATGTATAATAGAGTATAACCGTTACTTAAAAGAAGTCTGAATGTTGTTGGAAA
AGAAAATAGTTAAATTACTATCCCTAACCGAATGAAATTAGCCTTGCCTTACCTGTCATGGTAAGTAA
TTATTCTGCACTGTTGAACTTGTGAAACATTCTGAGTTGTTGTCATTCTGTAACAGTC
TCGAACTAGGCCCTAAAAACATCGTAACGAAAAGGCCAGCGAGGCAAATTCTGATTGATTGAATCTATATT
TTCTTAAAAGTCAAGGGTCTATATTGTGAGTAAATTAAATTACATTGAGTTGTTGCTAAGAGGTAG
TAAATGTAAGAGAGTACTGGTCCTCAGTAGTGAAGTATTCTCATAGTGCAGCTTATTATCTCCAGGATGTT
TTTGTGGCTGTATTGATTGATATGTGCTTCTGATTCTGCTAATTCAACCATATTGAATAATGTGATC
AAAGTC

FIGURE 6

><subunit 1 of 1, 737 aa, 1 stop

><MW: 78475, pI: 5.09, NX(S/T): 11

MQPRRAQAPGAQLLPALALLLLLLGAGPRGSSLANPVPAAPLSAPGPCAQPCRNGGVCTSR
PEPDHQHPAPAGEPGYSCTCPAGISGANCQLVADPCASNPCHGNCSSSSSSDGYLCICN
EGYEGPNCEQALPSLPATGWTEMAPRQLQPVATQEPDKILPRSQATVLPWTQPKTGQKV
VEMKWDQVEVIPDIACGNASSNSSAGGLVSVFEPQNTSVKIRQDATASLILLWKTATGFQ
QCSLIDGRSVTPLQASGLLVLEEMLALGNNHFIGFVNDSVTKSIVALRTLTVVKVSTCVPG
ESHANDLECSGKGKCTTKPSEATFSCTEEQYVGTFCCEYDACPQRKPCQNNASCIDANEKQD
GSNFTCVCLPGYTGELCQSKIDYCILDPCRNGATCISSLSGFTQCPEGYFGSACEEKVDPC
ASSPCQNNGTCYVDGVHFTCNCSPGFTGPTCAQLIDFCALSPCAHGTCSRSGTSYKCLCDPG
YHGLYCEEYNECLSAAPCLNAATCRDLVNGYECVCLAEYKGTHCELYKDPCANVSLNGATC
DSDGLNGTCICAPGFTGEEDIDINECDSNPCHGGSCLDQPNNGYNCHCPHWVGANCEIHL
QWKSGHMAESLTNMPRHSLYIIIGALCVAFILMLIILIVGICRISRIEYQGSSRPAYEEFYN
CRSIDSEFSNAIASIRHARFGKKSRPAMYDVSPIAYEDYSPDDKPLVTLIKTKDL

Signal sequence.

amino acids 1-28

Transmembrane domain.

amino acids 641-660

N-glycosylation sites.

amino acids 107-111, 204-208, 208-212, 223-227, 286-290, 361-365,
375-379, 442-446, 549-553, 564-568

Glycosaminoglycan attachment site.

amino acids 320-324

Tyrosine kinase phosphorylation sites.

amino acids 490-498, 674-682

N-myristylation sites.

amino acids 30-36, 56-62, 57-63, 85-91, 106-112, 203-209,
373-379, 449-455, 480-486, 562-568, 565-571

Amidation site.

amino acids 702-706

Aspartic acid and asparagine hydroxylation site.

amino acids 520-532, 596-608

EGF-like domain cysteine pattern signatures.

amino acids 80-92, 121-133, 336-348, 378-390, 416-428, 454-466,
491-503, 529-541, 567-579, 605-617

FIGURE 7

CTCTGGAAGGTACGGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAAGTGTGA
CCCCCCTTCAGGCTTCAGGGGGACTGGTCCTCCTGGAGGAGATGCTCGCCTGGGAATA
ATCACTTATTGGTTTGTGAATGATTCTGTGACTAAGTCTATTGTGGCTTGCCTTAAC
CTGGTGGTGAAGGTACGCACCTGTGTGCCGGGGAGAGTCACGCAAATGACTTGGAGTGTTC
AGGAAAAGGAAAATGCACCAACGAAAGCCGTCAAGAGGCAACTTTCTGTACCTGTGAGGAGC
AGTACGTGGTACTTCTGTGAAGAATACGATGCTGCCAGAGGAAACCTGCCAAACAAAC
GCGAGCTGTATTGATGCAAATGAAAAGCAAGATGGAGCAATTTCACCTGTGTTGCCTTCC
TGGTTATACTGGAGAGCTTGCCAACCGAACTGAGATTGGAGCGAACGACCTACACCGAACT
GAGATAGGGAG

FIGURE 8

CTCTGGAAGGTACGGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAAGTGTGA
CCCCCCTTCAGGCTTCAGGGGACTGGTCCTCCTGGAGGAGATGCTCGCCTGGGAATA
ATCACTTATTGGTTTGTGAATGATTCTGTGACTAAGTCTATTGTGGCTTGCCTTAAC
CTGGTGGTGAAGGTCAACCTGTGTGCCGGGGAGAGTCACGCAAATGACTGGAGTGTTC
AGGAAAAGGAAAATGCACCAACGAAGCCGTCAAGAGCAACTTTCTGTACCTGTGAGGAGC
AGTACGTGGTACTTCTGTGAAGAATACGATGCTGCCAGAGGAAACCTGCCAAAACAAC
GCGAGCTGTATTGATGCAAATGAAAAGCAAGATGGAGCAATTTCACCTGTGTTGCCTTCC
TGGTTATACTGGAGAGCTTGCCAACCGAACTGAGATTGGAGCGAACGACCTACACCGAACT
GAGATAGGGGAG

FIGURE 9

GCTGAGTCTGCTGCTCCTGCTGCTGCTGCTCCAGCCTGTAACCTGTGCCTACACCACGCCAG
GCCCCCCCAGAGCCCTACCACGCTGGCGCCCCAGAGCCCACACCATGCCGGCACCTAC
GCTCCCTGACCACACTCAGTAGTCCCAGCACCCAGGGCCTGCAAGAGCAGGCACGGCCCT
GATGCGGGACTTCCCGCTCGTGGACGGCCACAACGACCTGCCCCTGGTCCTAAGGCAGGTTT
ACCAGAAAGGGCTACAGGATGTTAACCTGCGCAATTTCAGCTACGCCAGACCAGCCTGGAC
AGGCTTAGAGATGGCCTCGTGGCGCCAGTTCTGGTCAGCCTATGTGCCATGCCAGACCCA
GGACCGGGATGCCCTGCGCCTCACCTGGAGCAGATTGACCTCATGCCGATGTGCGCT
CCTATTCTGAGCTGGAGCTTGTGACCTCGGCTAAAGCTCTGAACGACACTCAGAAATTGGCC
TGCCTCATCGGTAGAGGGTGGCCACTCGCTGGACAATAGCCTCTCCATCTTACGTACCTT
CTACATGCTGGAGTGCCTACCTGACGCTCACCCACACCTGCAACACACCCCTGGCAGAGA
GCTCCGCTAAGGGCTTACCTTCTACAACACATCAGGGCTGACTGACTTTGGTGAG
AAGGTGGTGGCAGAAATGAACCGCCTGGCATGATGGTAGACTTATCCCATGTCTCAGATGC
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GTCCACTGTGGCAGATCACTCGACCACATCAAGGCTGTCAATTGGATCCAAGTTCATCGGA
TTGGTGGAGATTATGATGGGCCGGCAAATTCCCTCAGGGCTGGAAGACGTGTCCACATAC
CCGGTCTGATAGAGGAGTTGCTGAGTCGTGGCTGGAGTGAGGAAGAGCTTCAGGGTGTCC
TCGTGAAACCTGCTGGGTCTTCAGACAAGTGGAAAAGGTACAGGAAGAAAACAATGGC
AAAGCCCCCTGGAGGACAAGTTCCGGATGAGCAGCTGAGCAGTTCTGCCACTCCGACCTC
TCACGTCTGCGTCAGAGACAGAGTCTGACTTCAGGCCAGGAACACTGAGATTCCCATACA
CTGGACAGCCAAGTTACCAAGCAGTCAGTCAGTCAGAGTCCTCCCCACATGGCCCCAG
TCCTTGCAGTTGTGGCACCTTCCAGTCCTATTCTGTGGCTCTGATGATGACCCAGTTAGTCC
TGCCAGATGTCACTGTAGCAAGCCACAGACACCCACAAAGTTCCCTGTTGTGCAGGCACA
AATATTCTGAAATAATGTTGGACATAG

FIGURE 10

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA35595
<subunit 1 of 1, 433 aa, 1 stop
<MW: 47787, pI: 6.11, NX(S/T): 5
MPGTYAPSTTLSSPSTQGLQEQRALMRDFPLVDGHNDLPLVLRQVYQKGLQDVNLRNFSYGT
QTSLDRLRDGLVGAQFWSAYVPCQTQDRDALRLTLEQIDLIRRMCASYSELELVTSAKALND
TQKLAACLIGVEGGHSLDNSLSILRTFYMLGVRYLTLTHTCNTPWAESSAKGVHSFYNNISGL
TDFGEKVVAEMNRLGMMVDSLHVSARALEVSQAPVIFSHSAARGVCNSARNVPDDILQ
LLKKNGGVMVSLSMGVIQCNP SANVSTVADHFDHIKAVIGSKFIGIGG DYDGAGKFPQGLE
DVSTYPV LIEELLSRGWSEEELQGVLRGNLLRVFRQVEKVQEE NKWQS PLEDKFPDEQLSSS
CHSDLSRLRQRQSLTSGQELTEIPIHWTAKLPAKWSVSESSPHMAPVLA VVATFPV LILWL
```

N-glycosylation sites.

amino acids 58-62, 123-127, 182-186, 273-277

N-myristoylation sites.

amino acids 72-78, 133-139, 234-240, 264-270, 334-340, 389-395

Renal dipeptidase active site.

amino acids 134-157

FIGURE 11

AAAACCTATAAATATTCCGGATTATTCAACCGTCCCACCATCGGGCGCGGATCCGCGGCCG
CGAATTCTAAACCAACATGCCGGCACCTACGCTCCCTGACCACACTCAGTAGTCCCAGCA
CCCAGGGCCTGCAAGAGCAGGCACGGGCCCTGATCGGGACTTCCGCTCGGACGGCAC
AACGACCTGCCCTGGTCCTAAGGCAGGTTACCAGAAAGGGCTACAGGATGTTAACCTGCG
CAATTTCAGCTACGCCAGACCCAGCCTGGACAGGTTAGAGATGGCCTCGTGGCGCCAGT
TCTGGTCAGCCTATGTGCCATGCCAGACCCAGGACGGGATGCCCTGCCTCACCTGGAG
CAGATTGACCTCATGCCGCATGTGCTCCTATTCTGAGCTGGAGCTTGTGACCTCGGC
TAAAGCTCTGAACGACACTCAGAAATTGGCCTGCCTCATCGGTGTAGAGGGTGGCACTCGC
TGGACAATAGCCTCTCCATCTTACGTACCTTACATGCTGGAGTGCCTACCTGACGCTC
ACCCACACCTGCAACACACCCCTGGCAGAGAGCTCCGCTAAGGGCGTCCACTCCTCTACAA
CAACATCAGCGGGCTGACTGACTTTGGTGAGAAGGTGGCAGAAATGAACCGCCTGGCA
TGATGGTAGACTTATCCCATGTCTCAGATGCTGTGGCACGGCGGCCCTGGAAGTGTACAG
GCACCTGTGATCTTCTCCACTCGGCTGCCGGGTGTGCAACAGTGCTCGGAATGTTCC
TGATGACATCCTGCAGCTCTGAAGAAGAACGGTGGCGTGTGATGGTGTCTTGCCATGG
GAGTAATACAGTCAACCCATCAGCCAATGTGTCCACTGTGGCAGATCACTCGACCACATC
AAGGCTGTCATTGGATCCAAGTTCATCGGGATTGGTGAGATTATGATGGGCCGGCAAATT
CCCTCAGGGCTGGAAGACGTGTCCACATACCCGGCCTGATAGAGGAGTTGCTGAGTCGTG
GCTGGAGTGAGGAAGAGCTTCAGGGTGTCTCGTGGAAACCTGCTGCGGGCTTCAGACAA
GTGGAAAAGGTACAGGAAGAAAACAATGGCAAAGGCCCTGGAGGACAAGTCCGGATGA
GCAGCTGAGCAGTTCTGCCACTCCGACCTCTCACGTCTCGTCAGAGACAGAGTCTGACTT
CAGGCCAGGAACTCACTGAGATTCCCATACACTGGACAGCCAAGTTACCAAGCCAAGTGGTCA
GTCTCAGAGTCCTCCCCCACCCTGACAAAACACATGCCACCGTGCCAGCACCTGA
ACTCCTGGGGGACCGTCAGTCTCCTCTCCCCAAAACCCAAGGACACC

FIGURE 12

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA35872
><subunit 1 of 1, 446 aa, 0 stop
><NX (S/T) : 5
MPGTYAPSTTLSSPSTQGLQEQRALMRDFPLVDGHNDLPLVLRQVYQKGLQDVNLRNFSYG
QTSLDRLRDGLVGAQFWSAYVPCQTQDRDALRLTLEQIDLIRRMCAZYSELELVTSAKALND
TQKLAACLIGVEGGHSLDNSLSILRTFYMLGVRYLTLCNTPWAESSAKGVHSFYNNISGL
TDFGEKVVAEMNRLGMMVDLSHVSDAVARALEVSQAPVIFSHSAARGVCNSARNVPDDILQ
LLKKNGGVMVMSLMGVIQCNPSANVSTVADHFDHIKAVIGSKFIGIGGDYDGAGKFPQGLE
DVSTYPVLIELLSRGWSEEELQGVLRGNLLRVFRQVEKVQEENKWQSPLEDKFPDEQLSSS
CHSDLRLRQRQSLTSGQELTEIPIHWTAKLPAKWSVSESSPHPDKTHTCPPCPAPELLGGP
SVFLFPPPKD

FIGURE 13

CGCCCAGCGACGTGCGGGCGGCCTGGCCCGGCCCTCCCGCGCCCGGCCTGCGTCCCGCGCC
CTGCGCCACCGCCGCCGAGCGCAGCCCGCCGCCGGCAGCGCCGGCCCCATGCCC
GCCGGCCGCCGGGGCCCCGCCGCCAATCGCGCGGCCGCCGCCGCTGCTGCCCTGCT
GCTGCTGCTCTCGCTCCTCGGGCGCCGAGCCGGATCAGGAGCCCACACAGCTGTGATCA
GTCCCCAGGATCCCACGCTTCTCATCGGCTCCTCCCTGCTGGCACCTGCTCAGTGCACGGA
GACCCACCAGGAGCCACCGCCGAGGGCCTACTGGACCCCTAACGGCGCCGCCGCCCC
TGAGCTCTCCCGTGTACTCAACGCCCTCACCTGGCTCTGGCCCTGGCAACCTCAATGGGT
CCAGGCAGCGGTGGGGACAACCTCGTGTGCCACGCCGTGACGGCAGCATTGGCTGGC
TCCTGCCTCTATGTTGGCCTGCCCTGGACAGAGAAACCGTCAACATCAGCTGCTGGTCCAAGAA
CATGAAGGACTTGACCTGCCGCTGGACGCCAGGGGCCACGGGAGACCTTCCTCACACCA
ACTACTCCCTCAAGTACAAGCTTAGGTGGTATGCCAGGACAACACATGTGAGGAGTACAC
ACAGTGGGGCCCCACTCCTGCCACATCCCCAAGGACCTGGCTCTTACGCCCTATGAGAT
CTGGGTGGAGGCCACCAACCGCCTGGCTCTGCCGCTCCGATGTACTCACGCTGGATATCC
TGGATGTGGTGACCACGGACCCCCCGCCGACGTGACGTGAGCCGCTGGGGCCCTGGAG
GACCAGCTGAGCGTGCCTGGGTGTCGCCACCGCCCTCAAGGATTCCCTTTCAAGCCAA
ATACCAGATCCGCTACCGAGTGGAGGACAGTGTGGACTGGAAGGTGGACGATGTGAGCA
ACCAGACCTCCTGCCGCTGGCCGGCTGAAACCCGGCACCGTGTACTCGTCAAGTGC
TGCAACCCCTTGGCATCTATGGCTCCAAGAAAGCCGGATCTGGAGTGAGTGGAGCCACCC
CACAGCCGCTCCACTCCCCCAGTGAGCGCCGGGCCGGCGGGCGTGCACCGC
GGGGCGGAGAGCCGAGCTGGGGCCGGTGCAGCGAGCTAAGCAGTTCTGGCTGGCTC
AAGAAGCAGCGTACTGCTCCAACCTCAGCTTCCGCTCTACGACCGAGTGGCGAGCCTGGAT
GCAGAAAGTCGCACAAGACCCGCAACCAGGACGGAGGGATCCTGCCCTGGCAGACGGGCA
CGCGAGAGGTCTGCCAGATAAGCTGTAGGGCTCAGGCCACCCCTGCCACGTGGAGA
CGCAGAGGCCAACCCAAACTGGGCCACCTCTGTACCCACTTCAGGGCACCTGAGGCCAC
CCTCAGCAGGAGCTGGGTGGCCCTGAGCTCCAACGCCATAACAGCTCTGACTCCCACGT
GAGGCCACCTTGGGTGCACCCAGTGGGTGTGTGTGAGGGTTGGTTGAGTTGC
CTAGAACCCCTGCCAGGGCTGGGGTGAGAAGGGAGTCATTACTCCCCATTACCTAGGGCC
CCTCCAAAAGAGTCCTTTAAATAATGAGCTATTAGGTGCTGTGATTGTGAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAACAAAAAAA

FIGURE 14

><ss.DNA38113

><subunit 1 of 1, 422 aa, 1 stop

><MW: 46302, pI: 9.42, NX(S/T): 6

MPAGRRGPAAQSARRPPPLLPLLLLCLVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATCSV
HGDPPGATAEGLYWTLNRRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARDGSIL
AGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTGAHGETFLHTNYSLKYLWYQDNTCEE
YHTVGPNSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPDVHVSRVGG
LEDQLSVRVSPPALKDFLFQAKYQIRYRVEDSVDKVVDDVSNQTSCRLAGLKPGTVYFVQ
VRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGACEPRGGEPPSGPVRRELKQFLG
WLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILPSGRRGTARGPAR

Signal sequence.

amino acids 1-30

Transmembrane domain.

amino acids 44-61

N-glycosylation sites.

amino acids 92-96, 104-108, 140-144, 168-172, 292-296, 382-386

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 413-417

N-myristoylation sites.

amino acids 30-36, 37-43, 73-79, 121-127, 179-185, 218-224,
300-306, 317-323, 320-326, 347-353, 355-361, 407-413

Amidation site.

amino acids 3-7, 79-83, 411-415

Growth factor and cytokines receptors family signature 2.

amino acids 325-331

FIGURE 15

CCACCGCGTCCGCTGGTGTAGATCGAGCAACCCTCTAAAAGCAGTTAGAGTGGTAAAAAA
AAAAAAAAACACACCAACCGCTCGCAGCCACAAAAGGG**A**TGAAATTCTCTGGACATCCTC
CTGCTTCTCCCGTTACTGATCGTCTGCTCCCTAGAGTCCTCGTGAAGCTTTTATTCTAA
GAGGAGAAAATCAGTCACCGCGAAATCGTGTGATTACAGGAGCTGGCATGGAATTGGGA
GAUTGACTGCCTATGAATTGCTAAACTTAAAGCAAGCTGGTCTCTGGATATAAATAAG
CATGGACTGGAGAACAGCTGCCAATGCAAGGACTGGTGCCAGGTTACACCTTGT
GGTAGACTGCAGCAACCGAGAAGATATTACAGCTCTGCAAAGAAGGTGAAGGCAGAAATTG
GAGATGTTAGTATTAGTAAATAATGCTGGTAGTCTATACATCAGATTGTTGCTACA
CAAGATCCTCAGATTGAAAAGACTTTGAAGTTAATGTACTTGACACATTCTGGACTACAAA
GGCATTCTTCCTGCAATGACGAAGAATAACCATTGCCATTGTCACTGTGGCTCGCAG
CTGGACATGTCTCGGTCCCCCTTACTGGCTACTGTTCAAGCAAGTTGCTGCTGTTGGA
TTTCATAAAACTTGACAGATGAACGGCTGCCTACAAATAACTGGAGTCAAAACAACATG
TCTGTGTCCTAATTGTAACACTGGCTCATCAAAATCCAAGTACAAGTTGGACCCA
CTCTGGAACCTGAGGAAGTGGTAAACAGGCTGATGCATGGATTCTGACTGAGCAGAAGATG
ATTTTATTCCATCTTCTATAGCTTTTAACAACATTGAAAGGATCCTCCTGAGCGTT
CCTGGCAGTTTAAAACGAAAATCAGTTAAGTTGATGCAGTTATTGGATATAAAATGA
AAGCGCAA**TAA**GCACCTAGTTCTGAAAATGATTACAGGTTAGGTTGATGTCATCTA
ATAGTGCCAGAATTAAATGTTGAACCTCTGTTCTAATTATCCCCATTCTCAATA
TCATTGGAGGCTTGGCAGTCTTCATTACTACCACCTGTTCTTAGCCAAAAGCTGATT
ACATATGATATAAACAGAGAAATACCTTAGAGGTGACTTAAGGAAAATGAAGAAAAAGAA
CCAAAATGACTTATTAAAATAATTCCAAGATTATTGGCTCACCTGAAGGCTTGCAA
ATTGTACCATACCGTTATTAAACATATATTATTGATTGACTTAAATTGTTG
ATAATTGTGTTCTTCTGTTCTACATAAAATCAGAAACTTCAGCTCTCAATGGTAGGTT
TGAAGGACTATATCTAGGGTATTTCACAATGAATATCATGAACCTCTCAATGGTAGGTT
ATCCTACCCATTGCCACTCTGTTCTGAGAGATACCTCACATTCAATGCCAACATTCT
GCACAGGGAAGCTAGAGGTGGATACACGTGTTGCAAGTATAAAAGCATCACACTGGATT
GAGAATTGAGAGAATGTACCCACAAATGGCAGCAATAATAATGGATCACACTTAAAAAAA
AA
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 16

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</usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA34436
<subunit 1 of 1, 300 aa, 1 stop
<MW: 32964, pI: 9.52, NX(S/T): 1
MKFLLDILLLPPLLIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK
LVLWDINKHGLEETAAKCKGLGAKVHTFVVDCSNREDIYSSAKVKAEIGDVSILVNNAGVV
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNGHIVTVASAAGHVSVPFLLAYC
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVVNRLMH
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMKAQ
```

Signal sequence.

amino acids 1-19

Transmembrane domain.

amino acids 170-187

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 30-34, 283-287

N-myristoylation sites.

amino acids 43-49, 72-78, 122-128, 210-216

FIGURE 17

GAAGTAGTTCTCTGGAGTCTGGAGGAGGAAAGCGGAGCCGGCAGGGAGCGAACCAAGGACTG
GGGTGACGGCAGGGCAGGGGGCGCTGGCCGGGAGAAGCGCAGGGCTGGAGCACCAAA
CTGGAGGGTCCGGAGTAGCGAGCGCCCCGAAGGAGGCCATGGGGAGCCGGAGGGGGACT
GCGAGAGGACCCGGCGTCCGGCTCCGGTGCAGCGCTATGAGGCCACTCCTCGTCTGC
TGCTCCTGGCCTGGCGGCCGGCTGCCCGGACTGGACGACAACAAGATCCCCAGCCTCTGC
CCGGGGCACCCGGCCTCCAGGCACGCCGGGCCACCATGGCAGCCAGGGCTGCCGGCG
CGATGGCCCGACGGCCCGACGGCGGCCGGCTCCGGAGAGAAAGGCAGGGCG
GGCCGGGACTGCCGGGACCTCGAGGGGACCCGGCCGAGGAGAGGCCGGACCCGG
CCACCGGGCCTGCCGGGAGTGCTCGGTGCCTCCCGATCCGCTTCAGGCCAAGCGCTC
CGAGAGCCGGTGCCTCCGCCGTCTGACGCACCCCTGCCCTCGACCGCGTGCCTGGTAACG
AGCAGGGACATTACGACGCCGTACCCGAAGTTCACCTGCCAGGTGCCTGGGTCTACTAC
TTCGCCGTCCATGCCACCGTCTACCGGGCAGCCTGCAGTTGATCTGGTAAGAATGGCGA
ATCCATTGCCCTTTCTTCAGTTTCGGGGGTGGCCAAGCCAGCCTCGCTCTCGGGG
GGCCATGGTGAGGCTGGAGGCTGAGGACCAAGTGTGGTGCAGGTGGTGTGGTACTAC
ATTGGCATCTATGCCAGCATCAAGACAGACAGCACCTCTCCGGATTCTGGTACTCCGA
CTGGCACAGCTCCCCAGTCTTGCTTAGTGCCACTGCAAAGTGAGCTATGCTCTCACTCC
TAGAAGGAGGGTGTGAGGCTGACAACCAGGTATCCAGGAGGGCTGGCCCCCTGGAATATT
GTGAATGACTAGGGAGGTGGGTAGAGCACTCTCCGTCTGCTGGCAAGGAATGGAAC
AGTGGCTGTCTGCCATCAGGTCTGGCAGCATGGGGCAGTGGCTGGATTCTGCCAAGACCA
GAGGAGTGTGCTGTGCTGGCAAGTGTAAAGTCCCCAGTTGCTCTGGTCCAGGAGGCCACGGT
GGGGTGCCTCTTCCCTGGTCTCTGCTCTGGATCCTCCCCACCCCTCTGCTCCTGGG
GCCGGCCCTTTCTAGAGATCACTCAATAAACCTAAGAACCCCTCATAAAAAAAAAAAAAA
AAAAAAAAAAAAAA

FIGURE 18

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40592
><subunit 1 of 1, 243 aa, 1 stop
><MW: 25298, pI: 6.44, NX(S/T): 0
MRPLLVLLLLGLAAGSPLLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPGAP
GEKGEGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSDAPLP
FDRV LVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFFQFFGGWP
KPASLSGGAMVRLEPEDQVWVQVGVDYIGIYASI KTDSTFSGFLVYSDWHSSPVFA
```

Signal sequence.

amino acids 1-15

N-myristoylation sites.

amino acids 11-17, 68-74, 216-222

Cell attachment sequence.

amino acids 77-80

FIGURE 19

CTCTTTGTCCACCAGCCCAGCCTGACTCCTGGAGATTGTGAATAGCTCCATCCAGCCTGAG
AAACAAGCCGGGTGGCTGAGCCAGGCTGTGCACGGAGCACCTGACGGGCCAACAGACCCAT
GCTGCATCCAGAGACCTCCCTGGCCGGGGCATCTCCTGGCTGTGCTCCTGGCCCTCCTTG
GCACCACCTGGGAGAGGTGTGGCCACCCAGCTGCAGGAGCAGGCTCCGATGGCCGGAGCC
CTGAACAGGAAGGAGAGTTCTTGTCTCCTCTCCCTGCACAACCGCCTGCGCAGCTGGTCCA
GCCCTGCGGCTGACATGCGGAGGCTGGACTGGAGTGACAGCCTGGCCAAGTGGCTCAAG
CCAGGGCAGCCCTGTGGAATCCAACCCGAGCCTGGCATCCGGCTGTGGCGCACCTG
CAAAGTGGCTGGAACATGCAGCTGCTGCCCGGGCTTGGCTCCTTGTGAAGTGGTCAG
CCTATGGTTGCAGAGGGCAGCGGTACAGCCACGCCAGGAGAGTGTGCTCGAACGCCA
CCTGCACCCACTACACGAGCTCGTGTGGCCACCTCAAGCCAGCTGGCTGTGGCGGCAC
CTGTGCTCTGCAGGCCAGACAGCGATAGAACGCCTTGCTGTGCCTACTCCCCGGAGGCAA
CTGGGAGGTCAACGGGAAGACAATCATCCCCTATAAGAAGGGTGCCTGGTGTGCTCTGCA
CAGCCAGTGTCTCAGGCTGCTCAAAGCCTGGACCATGCAGGGGGCTGTGAGGTCCCC
AGGAATCCTTGTGCGCATGAGCTGCCAGAACCATGGACGTCTAACATCAGCACCTGCCACTG
CCACTGTCCCCCTGGCTACACGGCAGATACTGCCAAGTGAAGGTGCAGCCTGCAGTGTG
ACGGCCGGTCCGGGAGGAGGTGCTCGTGTGACATCGGCTACGGGAGGCCAG
TGTGCCACCAAGGTGCATTTCCCTCACACCTGTGACCTGAGGATCGACGGAGACTGCTT
CATGGTGTCTTCAGAGGCAGACACCTATTACAGAGCCAGGATGAAATGTCAGAGGAAAGGCG
GGGTGCTGCCAGATCAAGAGCCAGAAAGTGCAGGACATCCTCGCCTCTATCTGGGCCGC
CTGGAGACCACCAACGAGGTGACTGACAGTGACTTCAGGACAGGAACCTCTGGATCGGGCT
CACCTACAAGACCGCCAAGGACTCCTCCGCTGGGCCACAGGGAGCACCGCCCTCACCA
GTTTGCCCTTGGCAGCCTGACAACCACGGCTGGTGTGGCTGAGTGCTGCCATGGGTTT
GGCAACTGCGTGGAGCTGCAGGCTCAGCTGCCCTCAACTGGAACGACCAGCGCTGCAAAAC
CCGAAACCGTTACATCTGCCAGTTGCCAGGAGCACATCTCCGGTGGGCCAGGGTCC
GAGGCCTGACCACATGGCTCCCTGCCCTGCCCTGGAGCACCGGCTCTGCTTACCTGTCTGC
CCACCTGTCTGGAACAAGGGCAGGTTAAGACCACATGCCTCATGTCAAAGAGGTCTCAGA
CCTTGCACAATGCCAGAAGTTGGCAGAGAGAGGCAGGGAGGCCAGTGAGGGCCAGGGAGTG
AGTGTAGAAGAAGCTGGGCCCTCGCCTGCTTGTGGAAAGATGGCTTCAATTAGA
TGGCGAAGGAGAGGACACCGCCAGTGGTCAAAAGGCTGCTCTTCCACCTGGCCAGAC
CCTGTGGGCAGCGGAGCTCCCTGTGGCATGAACCCACGGGTATTAAATTATGAATCAG
CTGAAAAA

FIGURE 20

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</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44176
<subunit 1 of 1, 455 aa, 1 stop
<MW: 50478, pI: 8.44, NX(S/T): 2
MLHPETSPGRGHLLAVLLALLGTTWAEVWPPQLQEAPMAGALNRKESFLLSLHNRLRSWV
QPPAADMRRLDWSDSLAQLAQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASFVEVV
SLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCRHLCAGQTAIEAFVCAYSPGG
NWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNPCRMSQNHGRLNISTCH
CHCPCPGYTGRYQVRCSDLQCVHGRFREEECSCVCDIGYGGAQCATKVHFFHTCDLRIDGDC
FMVSSEADTYYRARMKCQRKGGVLAQIKSQKVQDILAFYLRLETTNEVTDSDFETRNFWIG
LTYKTAKDSFRWATGEHQAFTSFAFGQPDNHGLVWLSAAMGFGNCVELQASAAFNWNDQRCK
TRNRYICQFAQEHI SRWGP GS
```

Signal sequence.

amino acids 1-26

Transmembrane domain.

amino acids 110-124

N-glycosylation sites.

amino acids 144-148, 243-247

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 45-49

N-myristylation sites.

amino acids 22-28, 99-105, 131-137, 201-207, 213-219, 287-293,
288-294, 331-337, 398-404

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 204-215

EGF-like domain cysteine pattern signature.

amino acids 249-261, 280-292

C-type lectin domain signature.

amino acids 417-442

FIGURE 21

CGGACGCGTGGCTGGCGCTGCAAAGCGTCTCCGCCGGTCCCCGAGCGTCCCGGCCCT
CGCCCCGCC**ATG**CTCTGCTGCTGGGCTGTGCCTGGGCTGTCCTGTGTGGGTCGCA
GAAAGAGGCGCAGAGCTGGGCCACTCTCGAGCAGGATGGACTCAGGGTCCCAGGCAAG
TCAGACTGTTGCAGAGGCTGAAAACCAACCTTGATGACAGAATTCTCAGTGAAGTCTACC
ATCATTTCCCGTTATGCCTTCACTACGGTTCTGCAGAATGCTGAACAGAGCTTCTGAAGA
CCAGGACATTGAGTCCAGATGCAGATTCCAGCTGCAGCTTCATCACCAACTTCACTATGC
TTATTGGAGACAAGGTGTATCAGGGCGAAATTACAGAGAGAGAAAAGAAGAGTGGTGTAGG
GTAAAAGAGAAAAGGAATAAAACCACAGAAGAAAATGGAGAGAGAGGGACTGAAATATTAG
AGCTTCTGCAGTGATTCCCAGCAAGGACAAAGCCGCTTTCTGAGTTATGAGGAGCTTC
TGCAGAGGCGCCTGGCAAGTACGAGCACAGCATCAGCGTGCAGCCAGCAGCTGTCCGGG
AGGCTGAGCGTGGACGTGAATATCCTGGAGAGCGCGGGCATCGCATCCCTGGAGGTGCTGCC
GCTTCACAAACAGCAGGCAGAGGGCAGTGGCGGGGAAGATGATTCTGGCCTCCCCAT
CTACTGTCAATTAAACCAAAATGAAACATTGCCAACATAATTAAACCTACTGTAGTACAA
CAAGCCAGGATTGCCAGAATGGAATTGGAGACTTATCATTAGATATGACGTCAATAG
AGAACAGAGCATTGGGACATCCAGGTTCTAAATGGCTATTGTGCACTACTTGCTCCTA
AAGACCTTCTCCTTACCCAGAATGTGGTATTGTGCTTGACAGCAGTGCTTCTATGGTG
GGAACCAAACCTCCGGCAGACCAAGGATGCCCTTCACAATTCTCCATGACCTCCGACCCCA
GGACCGTTTCAGTATCATTGGATTTCAACCGATCAAAGTATGGAAGGACCACTTGATAT
CAGTCACTCCAGACAGCATCAGGGATGGAAAGTGTACATTCAACATATGTCACCCACTGG
GGCACAGACATCAACGGGCCCTGCAGAGGGCATTAGGCTCCTCAACAAGTACGTGGCCCA
CAGTGGCATTGGAGACCGGAGCGTGTCCCTCATCGTCTCCTGACGGATGGAGGCCACGG
TCGGGGAGACGCACACCCCTCAAGATCCTCAACAACACCCGAGAGGCCGAGGCCAGTC
TGCATCTTCAACCATTGGCATCGAACGACGTGGACTTCAGGCTGCTGGAGAAACTGTCGCT
GGAGAACTGTGGCCTCACACGGCGCGTGCACGAGGAGGAGGACGCAGGCTCGCAGCTCATCG
GGTTCTACGATGAAATCAGGACCCCGCTCTCTGACATCCGCATCGATTATCCCCCAGC
TCAGTGGTGCAGGCCACCAAGACCCCTGTTCCCAACTACTTCAACGGCTGGAGATCATCAT
TGCAGGGAAAGCTGGACAGGAAGCTGGATCACCTGCACGTGGAGGTCAACGCCAGCAACA
GTAAGAAATTCACTCATCCTGAAGACAGATGTGCCTGTGCGGCCCTCAGAAGGCAGGGAAAGAT
GTCACAGGAAGCCCCAGGCCCTGGAGGCGATGGAGAGAGGGGACACCAACCACATCGAGCGTCT
CTGGAGCTACCTCACCACAAAGGAGCTGCTGAGCTCCTGGCTGCAAAGTACGATGAACCGG
AGAAGGAGCGGCTGCCAGCGGGCCAGGCCCTGGCTGTGAGCTACCGCTCCTCACTCCC
TTCACCTCCATGAAGCTGAGGGGCCGGTCCCACGCATGGATGGCCTGGAGGAGGCCACGG
CATGTCGGCTGCCATGGACCCGAACCGGTGGTGCAGAGCGTGCAGGAGCTGGCACGCAGC
CAGGACCTTGCTCAAGAACGCAAACCTCCGTCAAAAAAAAAACAAAACAAAACAAAAAGA
CATGGGAGAGATGGTGTGTTCTCCACCACTGGGATACGAT**G**AAAGATGCCACCT
GCAAGCCAGGAAGACGCCCTCACAGACACCATGTCGTGGCACCTGATCTGGACCTC
CCAGCCTCCAGAACTGTGAGAAATAATGTGTTAAGCTAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAA

FIGURE 22

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44192
<subunit 1 of 1, 694 aa, 1 stop
<MW: 77400, pI: 9.54, NX(S/T): 6
MLLLGLCLGLSLCVGSQEEAQSWGHSSEQDGLRVPRQVRLLQRLTKPLMTEFSVKSTIIS
RYAFTTVSCRMLNRASEDQDIEFQMQIIPAAAFITNFTMLIGDKVYQGEITEREKSGDRVKE
KRNKTEENGEKGTEIFRASAVIPSVDKAFFLSYEELLQRRLGKYEHSISVRPQQLSGRSL
VDVNILESAGIASLEVPLHNSRQRGSGRGEDESGPPPSTVINQNETFANIIFKPTVVQQAR
IAQNGILGDFIIRYDVNREQSIGDIQVLNGYFVHYFAPKDLPLPKNVVFVLDSSASMVGTK
LRQTKDALFTILHDLRPQDRFSIIGFSNRIKVWDHLISVTPDSIRDGKVYIHHMSPTGGTD
INGALQRAIRLLNKYVAHSGIGDRSVSLIVFLTDGKPTVGETHTLKILNNNTREAARGQVCIF
TIGIGNDVDFRLLEKLSLENCGLTRRVHEEEDAGSQLIGFYDEIRTPLLSDIRIDYPPSSVV
QATKTLFPNYFNGSEIIIAGKLVDRKLDHLHVEVTASNNSKKFIILKTDVPVRPQKAGKDVTG
SPRPGGDGEVDTNHIERLWSYLTTEKLLSSWLQSDDEPEKERLRQRAQALAVSYRFLTPFTS
MKLRGPVPRMDGLEEAHMSAAMGPEPVVQSVRGAGTQPGPLLKKPNSVKKQNKTKRHGR
DGVFPLHHLGIR
```

Signal sequence.

amino acids 1-14

N-glycosylation sites.

amino acids 97-101, 127-131, 231-235, 421-425, 508-512, 674-678

Glycosaminoglycan attachment sites.

amino acids 213-217, 391-395

N-myristoylation sites.

amino acids 6-12, 10-16, 212-218, 370-376, 632-638, 638-644

FIGURE 23

CGGACGCGTGGGTGCCGACATGGCGAGTGTAGTGCTGCCGAGCGGATCCCAGTGTGCGGC
GGCAGCGCGGGCGCGCGCCTCCCGGCTCCGGCTTGCTGCTCTCTCCGCCGCGG
CACTGATCCCCACAGGTGATGGCAGAATCTGTTACGAAAGACGTGACAGTGATCGAGGGA
GAGGTTGCGACCATCAGTTCCAAGTCAATAAGAGTGACGACTCTGTGATTCAAGCTACTGAA
TCCCAACAGGCAGACCATTATTCAGGGACTTCAGGCCTTGAAGGACAGCAGGTTTCACT
TGCTGAATTTCTAGCAGTGAACCTCAAAGTATCATTGACAAACGTCTCAATTCTGATGAA
GGAAGATACTTTGCCAGCTCTACCGATCCCCACAGGAAAGTTACACCACCATCACAGT
CCTGGTCCCACCACGTAATCTGATGATCGATATCCAGAAAGACACTGCAGGTGAAAGGTGAGG
AGATTGAAGTCAACTGCACTGCTATGCCAGCAAGCCAGCCACGACTATCAGGTGGTTCAA
GGGAACACAGAGCTAAAGCAAATCGGAGGTGGAAGAGTGGTCAGACATGTACACTGTGAC
CAGTCAGCTGATGCTGAAGGTGACAAGGAGGACGATGGGTCCCAGTGATCTGCCAGGTGG
AGCACCCCTGCCGTACTGAAACCTGCAGACCCAGCGGTATCTAGAAGTACAGTATAAGCCT
CAAGTGCACATTAGATGACTTATCCTCTACAGGCTTAACCCGGAAAGGGACCGCTTGA
GTTAACATGTGAAGCCATCGGAAGCCCCAGCCTGTGATGGTAACGGTGGAGAGTCGATG
ATGAAATGCCTCAACACGCCGTACTGTCTGGGCCAACCTGTTCATCAATAACCTAAACAAA
ACAGATAATGGTACATACCGCTGTGAAGCTCAAACATAGTGGGAAAGCTCACTCGGATTA
TATGCTGTATGTATACGATCCCCCACAACATCCCTCCACAACAACCACCA
CCACCACCACCACCACCATCCTTACCATCATCACAGATTCCGAGCAGGTGAAGAAGGC
TCGATCAGGGCAGTGGATCATGCCGTGATCGGTGGCGTGTGGCGGTGGTGGTGGTGGTGG
GCTGTGCTTGCATCATTCTGGGGCGCTATTTGCCAGACATAAGGTACATACTCACTC
ATGAAGCCAAAGGAGCCGATGACGCGAGCAGCAGACACAGCTATAATCAATGCAGAAGGA
GGACAGAACAACTCCGAAGAAAAGAAAGAGTACTTCATCTAGATCAGCCTTTGTTCAAT
GAGGTGTCCAATGCCCTATTAGATGATAAGAGACAGTGATATTGG

FIGURE 24

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</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA39518
<subunit 1 of 1, 440 aa, 1 stop
<MW: 48240, pI: 4.93, NX(S/T): 7
MASVVLPSGSQCAAAAAAAAPPGLRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISC
QVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSIISDEGRYFCQL
YTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKG
KSEVEEWSDMYTVTSQMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMT
YPLQGLTREGDALELTCEAIGKPQPVMTWVRVDEMPOHAVLSGPNLFINNLNKTDNGTYR
CEASNIVGKAHSYMLYVYDPPTI PPPTTTTTTTTTILTIITDSRAGEEGSIRAVDH
AVIGGVVAVVVFAMLCLLIIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEE
KKEYFI
```

Signal sequence.

amino acids 1-36

Transmembrane domain.

amino acids 372-393

N-glycosylation sites.

amino acids 65-69, 99-103, 111-115, 163-167, 302-306, 306-310,
430-434

Tyrosine kinase phosphorylation sites.

amino acids 233-240, 319-328

N-myristylation sites.

amino acids 9-15, 227-233, 307-313, 365-371, 376-382, 402-408,
411-417, 427-433, 428-432

FIGURE 25

GGGGCGGGTGGACCGGACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCTCGGGCCCGA
CCCGCCAGGAAAGACTGAGGCCGCGGCCCTGCCCGCCCGCTCCCTGCGCCGCCGCCCTC
CCGGGACAGAAGATGGCTCCAGGGTCCCTCTGCTGCTGCCGCTGCTCCCTGCTACTGGCCCT
GGGGCCTGGGTGCAGGGCTGCCATCCGGCTGCCAGTGCAGCCAGCACAGACAGTCTTCT
GCACTGCCGCCAGGGACCACGGTCCCCGAGACGTGCCACCCGACACGGTGGGCTGTAC
GTCTTGAGAACGGCATCACCATGCTGACGCAAGCAGCAGCTTGCCGGCTGCCGGCCTGCA
GCTCCTGGACCTGTCACAGAACCGAGATGCCAGCCTGCCCTGCCCGCCTGCTGCTGCTGG
ACCTCAGCCACAACAGCCTGCCCTGGAGGCCATCCTGGACACTGCCAACGTGGAG
GCGCTGCGGCTGGCTGGTCTGGGCTGCAGCAGCTGGACGAGGGCTCTCAGCCGCTGCG
CAACCTCACGACCTGGATGTGTCGACAACAGCAGCTGGAGCGAGTGCCACCTGTGATCCGAG
GCCTCCGGGCCTGACGCCCTGCCGGCAACACCCGATTGCCAGCTGCCGGCC
GAGGACCTGGCCGGCCTGGCTGCCCTGCAGGAGCTGGATGTGAGCAACCTAACGCTGCAGGC
CCTGCCTGGCAGCCTCTGGCCCTTCCCCCCTGCCCTGGAGCTGGCAGCTGCCGCAACC
CCTTCAACTGCGTGTGCCCTGAGCTGGTTGGCCCTGGGTGCGAGAGGCCACGTACA
CTGGCCAGCCCTGAGGAGACGCCACTTCCCCTGCAAGAACGCTGCCGGCTGCTCCT
GGAGCTTGAACCGCCGACTTGGCTGCCAGCCACCACAGCCACAGTGCCACCCA
CGAGGCCCGTGGTGGGGAGCCCACAGCCTGTCTAGCTGGCTCCTACCTGGCTTAGC
CCACAGGCCGGCCACTGAGGCCAGGCCCTCCACTGCCAACCGACTGTAGGGCC
TGTCCCCAGCCCCAGGACTGCCACCGTCCACCTGCCATGGGGCACATGCCACCTGG
GGACACGGCACCACCTGGCGTGTCTGTGCCCGAAGGCTTCAGGGCTGTACTGTGAGAGC
CAGATGGGCAGGGACACGGCCAGCCCTACACCAGTCAGCCGAGGCCACCACGGTCCCT
GACCCCTGGCATCGAGCCGGTGGAGCCCCACCTCCCTGCCGTGGGCTGCAGCGTACCTCC
AGGGAGCTCGTGCAGCTCAGGAGCCTCGTCACTATCGAACCTATCGGGCCCTGAT
AAGCGGCTGGTGACGCTGCCACTGCCCTGCCCTCGCTGAGTACACGGTCACCCAGCTGCG
GCCAACGCCACTTACTCCGTCTGTGTCATGCCATTGGGCCCGGGCGGGTGCCGGAGGGCG
AGGAGGCCTGCCGGGAGGCCATACACCCAGCCGTCACCTCAACCACGCCAGTCACC
CAGGCCCGCAGGGCAACCTGCCCTCATTGCCCGCCCTGCCCGGGTGCCTGGC
CGCGCTGGCTGCCGGTGGGGCAGCCTACTGTGTGCCGGGGGGCCATGGCAGCAGCGG
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CCCTGGAGCCAGGCCAGGCCAACAGAGGCCGGTGGAGAGGCCCTGCCAGCGGGTCTGA
GTGTGAGGTGCCACTCATGGCTTCCCAGGGCTGCCCTCCAGTCACCCCTCCACGCAAAGC
CCTACATCTAAGCCAGAGAGAGACAGGGCAGCTGGGCCGGCTCTCAGCCAGTGAAGATGGC
CAGCCCCCTCTGCTGCCACACCACGTAAGTCTCAGTCCAAACCTCGGGATGTGTGAGA
CAGGGCTGTGTGACCACAGCTGGCCCTGTTCCCTCTGGACCTCGGTCTCCTCATCTGTGAG
ATGCTGTGGCCAGCTGACGAGCCCTAACGTCCCCAGAACCGAGTGCCTATGAGGACAGTGT
CCGCCCTGCCCTCCGCAACGTGCAGTCCCTGGCACGGCGGGCCCTGCCATGTGCTGGTAAC
GCATGCCCTGGGCCCTGCTGGCTCTCCACTCCAGGCCGGACCCCTGGGGCCAGTGAAGGAAG
CTCCCGGAAAGAGCAGAGGGAGAGCGGGTAGGCCGGCTGTGACTCTAGTCTGGCCCCAGG
AAGCGAAGGAACAAAGAAACTGAAAGGAAGATGCTTAGGAACATGTTTGCTTTAA
AATATATATATATTATAAGAGATCCTTCCATTATTCTGGGAAGATGTTTCAAACCTC
AGAGACAAGGACTTGGTTTGTAAAGACAAACGATGATGATGAAGGCCTTGTAAAGAAAAA
ATAAAAAAAAAAA

FIGURE 26

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44804

<subunit 1 of 1, 598 aa, 1 stop

<MW: 63030, pI: 7.24, NX(S/T): 3

MCSRVPLLLPLLLLALGPGVQGCPSCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVFEN
GITMLDASSFAGLPGQLQLLDSQNQIASLRLPRLLLLLDSHNSLLALEPGILD TANVEALRL
AGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLRGLTRLRLAGNTRIAQLRPEDIA
GLAALQELDVSNLSQLALPGDLSGLFPRLRLLAAARNPFNCVCPLSWFGPWVRESHVTLASP
EETRCHFPPKNAGRLLLELDYADFGCPATTTATVPTTRPVVREPTALSSLAPTWLSPTAP
ATEAPSPPSTAPPTVGPVPQPQDCPPSTCLNGGTCHLGTRHHLACLCPEGFTGLYCESQMGQ
GTRPSPTPTVPRPPRSLTGIEPVSPSLRVGLQRYLQGSSVQLRSLRLTYRNLSGPDKRLV
TLRLPASLAEYTWTQLRPNATYSVCVMP LGPGRVPEGEEACGEAHTPPAVHSNAPVTQARE
GNLPLLIA PALAAVLLAALAAVGAAYCVRGRAMAAAQDKGQVGP GAGPLELEGVKVPLEP
GPKATEGGGEALPSGSECEVPLMGFPGPGLQSPLHAKPYI

Signal sequence.

amino acids 1-23

Transmembrane domain.

amino acids 501-522

N-glycosylation sites.

amino acids 198-202, 425-429, 453-457

Tyrosine kinase phosphorylation site.

amino acids 262-270

N-myristoylation sites.

amino acids 23-29, 27-33, 112-118, 273-279, 519-525, 565-571

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

EGF-like domain cysteine pattern signature.

amino acids 355-367

Leucine zipper pattern.

amino acids 122-144, 194-216

FIGURE 27

GGCACTAGGACAACCTTCTCCCTTCTGCACCACTGCCGTACCCCTACCCGCCACC
TCCTTGCTACCCACTCTTGAAACACAGCTGTTGGCAGGGTCCCCAGCTC**ATGCCAGCCTC**
ATCTCCTTCTGCTAGCCCCAAAGGGCCTCCAGGCAACATGGGGGCCAGTCAGAGAGC
CGGCACTCTCAGTTGCCCTGGTTGAGTTGGGGGAGCTCTGGGGCCGTGGCTTGCC
ATGGCTCTGCTGACCCAAACAAACAGAGCTGCAGAGCCTCAGGAGAGAGGTGAGCCGGCTGCA
GGGGACAGGAGGCCCTCCCAGAATGGGAAGGGTATCCCTGGCAGAGTCTCCGGAGCAGA
GTTCCGATGCCCTGGAAGCCTGGGAGAATGGGGAGAGATCCCGAAAAGGAGAGCAGTGCTC
ACCCAAAAACAGAAGAAGCAGCACTCTGTCCTGCACCTGGTTCCATTAAACGCCACCTCAA
GGATGACTCCGATGTGACAGAGGTGATGTGGCAACCAGCTCTTAGCGTGGAGAGGCCTAC
AGGCCAAGGATATGGTGTCCGAATCCAGGATGCTGGAGTTATCTGCTGTATAGCCAGGTC
CTGTTCAAGACGTGACTTCACCATGGTCAGGTGGTGTCTCGAGAAGGCCAAGGAAGGCA
GGAGACTCTATTCCGATGTATAAGAAGTATGCCCTCCACCCGACCGGGCTACAACAGCT
GCTATAGCGCAGGTGTCTCCATTTACACCAAGGGATATTCTGAGTGTCTAAATTCCCCGG
GCAAGGGCGAAACTTAACCTCTCCACATGGAACCTCCTGGGGTTGTGAAACT**TGATT**
GTGTTATAAAAAGTGGCTCCAGCTTGGAAAGACCAGGGTGGGTACATACTGGAGACGCCA
GAGCTGAGTATATAAGGAGAGGAATGTGCAGGAACAGAGGCATCTCCTGGGTTGGCTC
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CTTCTGTTCCCCATGGAGCTCCG

FIGURE 28

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</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52722
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ATSKDDSDVTEVMWQPALRRGRGLQAQGYGVRIQDAGVYLLYSQVLFQDVTFMGQVVSREG
QGRQETLFRCIRSMPSHPDRAYNSCYSAGVFHLHQGDILSVIIPRARAKLNLSPHGTFLGFVKL
```

Signal sequence.

amino acids 1-40

N-glycosylation site.

amino acids 124-128

Tyrosine kinase phosphorylation site.

amino acids 156-164

N-myristoylation site.

amino acids 36-42, 40-46, 179-185, 242-248

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 34-45

FIGURE 29

CACTTCTCCCTCTTCTGAGAAACCGCGCTTCCGCTTCTGGTCGCAGAGAC
CTCGGAGACCGCGCCGGGAGACGGAGGTGCTGTGGTGGGGGACCTGTGGCTGCTCGTA
CCGCCCCCCCACCCCTCTGCACTGCCGCCTCCGAAGACCTTTCCCTGCTCTGTT
TCCTCACCGAGTCTGTGCATGCCCGGACCTGCCGGAGGAGGCTGGCCGGAGA
TGCTCTAGGGCGGGAGGAGCAGGCCGGACGGAGGGCAGGAGGGCCGGCAGGAAGATGGC
TCCCGTGGACAGGGACTTTGCTGGCGTACTGCCGCCTTGCTTGCCTCTGGCCTGGT
CCTGAGTCGTGCCCCATGCCAGGGGAACAGCAGGAGTGGGAGGGACTGAGGAGCTGC
CGTCGCCTCCGGACCATGCCAGAGGGCTGAAGAACACATGAAAAAATACAGGCCAGTCAG
GACCAGGGCTCCCTGCTTCCGGTCTGCGCTGCTGTGACCCGGTACCTCCATGTACCC
GGCAGCCGCGTGCAGATCAACATCACTATCTGAAAGGGAGAAGGGTACCGCGGAG
ATCGAGGCCTCCAAGGGAAATATGGCAAAACAGGCTCAGCAGGGCAGGGCCACACTGGA
CCCAAAGGGCAGAAGGGCTCCATGGGGCCCTGGGAGCGGTGCAAGAGCCACTACGCCGC
CTTTTCGGTGGCCGAAGAAGCCCAGTCACAGCAACCACTACTACCAAGACGGTATCTCG
ACACGGAGTCGTGAACCTCTACGACCACTCAACATGTTACCGGCAAGTTCTACTGCTAC
GTGCCGGCCTCTACTTCTCAGCCTCACGTGACACCTGGAACCAGAAGGAGACCTACCT
GCACATCATGAAGAACGAGGAGGAGGTGGTATCTTCTCGCAGGTGGCAGCGCAGCA
TCATGCAAAGCCAGAGCCTGATGCTGGAGCTGCGAGAGCAGGACCAGGTGTGGTACGCC
TACAAGGGCGAACGTGAGAACGCCATCTCAGCGAGGAGCTGGACACCTACATCACCTCAG
TGGCTACCTGGTCAAGCACGCCACCGAGCCTAGCTGGCCGGCACCTCCTCTCGCC
ACCTCCACCCCTGCGCTGTGCTGACCCACCGCCTTCCCGATCCCTGGACTCCGACTC
CCTGGCTTGGCATTCACTGAGACGCCCTGCACACACAGAAAGCCAAGCGATCGGTGCTCC
CAGATCCCGAGCCTCTGGAGAGAGCTGACGGCAGATGAAATCACCAAGGGCGGGCACCCGC
GAGAACCCCTCTGGGACCTCCGCGGCCCTCTGCACACATCCTCAAGTGACCCGCACGGC
GAGACGGGGTGGCGGAGGGCTCCAGGGTGCAGGCCGGCTCAGTCCTGGAAATA
ATTAGGCAAATTCTAAAGGTCTAAAAGGAGCAAAGTAAACCGTGGAGGACAAAGAAAAGGG
TTGTTATTTGTCTTCCAGCCAGCCTGCTGGCTCCAAGAGAGAGGCCTTTCAGTTGAG
ACTCTGCTTAAGAGAACATCCAAAGTTAAAGCTCTGGGTCAAGGGAGGGCCGGGGCAGG
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GATGGGGCTGGGCCAGGCAGCCTCCAGGGACAGCTGAGCCCCCTGCCTGGC
TCCAGGTTGGTAGAACAGCCAGGGCTCCTGACAGTGGCCAGGGACCCCTGGTCCCCA
GGCCTGCAGATTTCTATGAGGGCAGAGCTCCTGGTACATCCATGTTGGCTCTGCTCC
ACCCCTGTGCCACCCAGGCCCTGGGGGTGGCTCCATGCCACCCCTGGCATCGCT
TTCTGTGCCGCCTCCCACACAAATGCCAGAGGCCAGGGCCCTGGCTCTGTTTT
TATAAAACACCTCAAGCAGCACTGCAGTCCTCCATCTCCTGGCTAAGCATCACCCT
CCACGTGTGTTGGTGGCAGCAAGGCTGATCCAGACCCCTCTGCCCAACTGCC
CATCCAGGCCTCTGACCACTAGCCTGAGAGGGCTTTCTAGGCTTCAGAGCAGGGAGAG
CTGGAAGGGCTAGAAAGCTCCGCTGTGTTCTCAGGCTCTGTGAGCCTCAGTC
AGACCAAGACTCAAGAGGAAGTACACGTCCAATCACCGTGTCAAGGATTCACTCTCAGGAGC
TGGGTGGCAGGAGAGGCAATAGCCCTGTTGCAATTGCAAGGACAGCTGGAGCAGGGTGGCG
GTGTCTCCACGGTCTCGCCCTGCCATGCCACCCAGACTCTGATCCAGGAACCC
ATAGCCCTCTCCACCTCACCCATGTTGATGCCAGGGTCACTCTGCTACCCGCTGGGCC
CCCAAACCCCCGCTGCCCTCTTCCCTCCCCCAGCTGGTTTGACTAATCCTGC
TTCCCTCTGGGCTGGCTGCCGGATCTGGGTCCCTAAGTCCCTCTCTTAAAGAACTT
CTGCGGGTCAGACTCTGAAGCCGAGTTGCTGTGGCGTGCCGGAGCAGAGGCCACACTC
GCTGCTTAAGCTCCCCAGCTTTCCAGAAAACATTAAACTCAGAATTGTGTTTCAA

FIGURE 30

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41234

><subunit 1 of 1, 281 aa, 1 stop

><MW: 31743, pI: 6.83, NX(S/T): 1

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TGPKGQKGSMGAPGERCKSHYAAFSVGRKKPMHSNHYYQTVIFDTEFVNLYDHFMFTGKFY
CYVPGLYFFSLNVHTWNQKETYLHIMKNEEEVILFAQVGDRSIMQSQSLMLELREQDQVWV
RLYKGERENAIFSEELDTYITFSGYLVKHATEP

Signal sequence.

amino acids 1-25

N-glycosylation site.

amino acids 93-97

N-myristoylation sites.

amino acids 7-13, 21-27, 67-73, 117-123, 129-135

Amidation site.

amino acids 150-154

Cell attachment sequence.

amino acids 104-107

FIGURE 31

GCGGAGCATCCGCTCGGGTCTCGCCGAGACCCCCGCGCGGATTGCCGGTCTTCCCGCG
GCGCGACAGAGCTGCCTCGCACCTGGATGGCAGCAGGGCGCCGGGTCTCTGACGCCA
GAGAGAAATCTCATCATCTGTCAGCCTTAAAGCAAACTAAGACCAGAGGGAGGATTAT
CCTTGACCTTGAAGACCAAAACTAAACTGAAATTAAAATGTTCTCGGGGGAGAAGGGAG
CTTGACTTACACTTGGTAATAATTGCTCCTGACACTAAGGCTGTCTGCTAGTCAGAATT
GCCTCAAAAAGAGTCTAGAAGATGTTGTCATTGACATCCAGTCATCTCTTCTAAGGGAATC
AGAGGCAATGAGCCGTATATACTTCAACTCAAGAAGACTGCATTAATTGCTGTTCAAC
AAAAAAACATATCAGGGACAAAGCATGTAACCTGATGATCTCGACACTCGAAAAACAGCTA
GACAACCCAACTGCTACCTATTTCTGCCCCAACGAGGAAGCCTGTCATTGAAACCAGCA
AAAGGACTTATGAGTTACAGGATAATTACAGATTTCATCTTGCACAGTCAAGCAGTCAC
CCAAGAGTACCCCAGGAAGATTCTCTTACATGGCCAATTTCACAAGCAGTCAC
TAGCCCCATCATCACACAGATTATTCAAAGCCCACCGATATCTCATGGAGAGACACACTTCT
CAGAAGTTGGATCCTCAGATCACCTGGAGAAACTATTAAAGATGGATGAAGCAAGTGCCA
GCTCCTTGCTTATAAGGAAAAGGCCATTCTCAGAGTTCACAAATTTCCTGATCAAGAAA
TAGCTCATCTGCTGCCCTGAAAATGTGAGTGCCTCCAGCTACGGTGGCAGTTGCTTCTCCA
CATACCACCTCGGCTACTCCAAAGCCGCCACCCCTCACCCACCAATGTTCAAGTGCAC
TTCTGGACTTCCCAGCCACAGCTGGCCACACAGCTCCACCTGTAACCACGTCACTCTC
AGCCTCCCACGACCCTCATTCTACAGTTTACACGGGCTGCCCTACACTCCAAGCAATG
GCTACAACAGCAGTCTGACTACCACCTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGA
AACCATAACCGTTACAGAAATCTCAAACTTAACACAGGAATGTGTATAACCCTA
CTGCACTTCTATGTCAAATGTGGAGTCTTCACTATGAATAAAACTGCTTCTGGAGGTT
AGGGAGGCCAGTCCAGGCAGTTCCCTCCAGGGCAGTGTCCAGAAAATCAGTACGGCCTTCC
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TCGTCTCCTGGTAGAATCCTTCGGAATCACTCCGAGAAACGTTACTCAAGACTGGAT
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TAGTAACCAGAAGCCAAATGCAATGAGTTCTGCTGACTTGCTAGTCTTAGCAGGAGGTTG
TATTGAAAGACAGGAAAATGCCCTTCTGCTTCTTCTTGGAGACAGAGTCTT
GCTCTGTTGCCAGGCTGGAGTGCAGTAGCACGATCTGGCTCTCACCGAACCTCCGTCTC
CTGGGTTCAAGCGATTCTCCTGCCTAGCCTCTAACGATCTGGGATTACAGGATGTGCCA
CCACACCTGGGTGATTTGTATTTAGTAGAGACGGGTTTACCCATGTTGGTCAGGCTG
GTCTCAAACCTCTGACCTAGTGAACCTCCCTCGGCTCCAAAGTGTGGATTACAGG
CATGAGCCACCACAGCTGGCCCCCTCTGTTTATGTTGGTTTGAGAAGGAATGAAGTG
GGAACCAAATTAGGTAATTGGTAATCTGCTCTAAATATTAGCTAAAACAAAGCTCT
ATGTAAAGTAATAAAAGTATAATTGCCATATAAAATTCAAACACTGGCTTTATGCAA
GAAACAGGTTAGGACATCTAGGTTCCAATTCACTCACATTCTGGTTCCAGATAAAACTCAAC
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CCAGATGTAGTCCCTCCAATTAAATATTGAATAAAATCTTTGTTACTCAA

FIGURE 32

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45410
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SLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHTDYSKPTDISWRDTLSQKFGSSDHLEKLF
KMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSATPKPATLL
PTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAATLQAMATTAVLTTTFQAP
TDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKTAWEGRASPGSSSQGSV
PENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRLDYILINGIYVDI
```

Signal sequence.

amino acids 1-25

Transmembrane domain.

amino acids 384-405

N-glycosylation sites.

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 415-419

Tyrosine kinase phosphorylation site.

amino acids 50-57

N-myristoylation sites.

amino acids 4-10, 48-54, 315-321

FIGURE 33

GCAGCCTGGAAAG**ATG**CGCCCATTGGCTGGTGGCCTGCTCAAGGTGGTTCGTGGCTTC
GCCTCCTTGTGTGCCTGGTATTGGGGTACCTGCTCGCAGAGCTCATTCCAGATGCACCCCT
GTCCAGTGCTGCCTATAGCATCCGCAGCATGGGAGAGGCCTGCCTCAAAGCTCCAGTCC
CCAAAAGGCAAAATGTGACCACTGGACTCCCTGCCATCTGACACCTATGCCTACAGGTTA
CTCAGCGGAGGTGGCAGAAGCAAGTACGCCAAATCTGCTTGAGGATAACCTACTTATGGG
AGAACAGCTGGAAATGTTGCCAGAGGAATAAACATTGCCATTGTCAACTATGTAACGGAA
ATGTGACAGCAACACGATGTTTGTATGTATGAAGGCGATAACTCTGGACCGATGACAAAG
TTTATTCAAGAGTGCTGCTCCAAATCCCTGCTCTCATGGTGACCTATGACGACGGAAGCAC
AAGACTGAATAACGATGCCAAGAATGCCATAGAAGCACTTGGAAAGTAAAGAAATCAGGAACA
TGAAATTCAAGGTCTAGCTGGGTATTATTGCAGCAAAGGCTTGGAACTCCCTCCGAAATT
CAGAGAGAAAAGATCAACCACCTGATGCTAAGAACACAGATATTCTGGCTGGCCTGCAGA
GATCCAGATAGAAGGCTGCATAACCAAAGAACGAAGC**TGA**CACTGCAGGGCCTGAGTAAAT
GTGTTCTGTATAACAAATGCAGCTGGAATCGCTCAAGAATCTTATTTCTAAATCCAACA
GCCCATATTGATGAGTATTGGGTTGTTGAAACCAATGAACATTGCTAGTTGTATCA
AATCTGGTACGCAGTATTTTATACCAAGTATTTATGTAAGATGTCAATTAGCAGGA
AACTAAAATGAATGGAAATTCTTAAAAAAA

FIGURE 34

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA46777
><subunit 1 of 1, 235 aa, 1 stop
><MW: 25982, pI: 9.09, NX(S/T): 2
MRPLAGGLLKVVFVVFASLC AWYSGYLLAELIPDAPLSSAAYSIRSIGERPVLKAPVPKRQK
CDHWTPCPSDTYAYRLLSGGGRSKYAKICFEDNLLMGEQLGNVARGINIAIVNYVTGNVTAT
RCFD MYEGDNGPMTKFIQSAAPKSLLFMVTYDDGSTRLNNDAKNAIEALGSKEIRNMKFRS
SWVFIAAKGLELPSEIQREKINHSDAKNNRYSGWPAEIQIEGCIPKERS
```

Signal sequence.

amino acids 1-20

N-glycosylation sites.

amino acids 120-124, 208-212

Glycosaminoglycan attachment site.

amino acids 80-84

N-myristylation sites.

amino acids 81-87, 108-114, 119-125